Genomic analysis of Bornean geckos (Gekkonidae: Cyrtodactylus) reveals need for updated taxonomy

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Abstract

Using molecular genetic data, recognised diversity within the gecko genus Cyrtodactylus has more than doubled, with many lineages that were once thought to be wide-ranging being delimitated into multiple independent species. On the Southeast Asian island of Borneo, there has been a recent renewed focus on reptile taxonomy, as genetic data have demonstrated a high amount of unrecognised biodiversity. We herein advance this taxonomic trend by delimiting three distinct species within the Cyrtodactylus consobrinus species complex: C. consobrinus, C. kapitensis sp. n., and C. hutan sp. n. To do so, we use a combination of ddRAD-seq and single-locus data, and morphological data. Using genomic data, we test species and population boundaries within the consobrinus species complex and show minimal population structure but high species-level diversity. Despite not finding uniquely diagnostic morphological characters to delimit the new species, we suggest a combination of characters that can be used to identify each lineage. Lastly, we use our data to comment on the status of C. malayanus, with indications that this lineage is also better considered a species complex. These data highlight the prevalence of unrecognised lineages on Borneo, many of which face threats due to increasing deforestation and other anthropogenic pressures.

KEYWORDS

ddRADseq, morphology, multispecies coalescent, population genetics, Southeast Asia, species delimitation